

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Grabstein, Kenneth
Paxton, Raymond
Pettit, Dean
- (ii) TITLE OF INVENTION: Antagonists of IL-15
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Immunex Corporation
(B) STREET: 51 University Street
(C) CITY: Seattle
(D) STATE: Washington
(E) COUNTRY: USA
(F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC Compatible
(C) OPERATING SYSTEM: Word for Windows 95, 7.0
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Malaska, Stephen L.
(B) REGISTRATION NUMBER: 32,655
(C) REFERENCE/DOCKET NUMBER: 2831
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 206-587-0430

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 489 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..342
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG	AGA	ATT	TCG	AAA	CCA	CAT	TTG	AGA	AGT	ATT	TCC	ATC	CAG	TGC	TAC	48
Met	Arg	Ile	Ser	Lys	Pro	His	Leu	Arg	Ser	Ile	Ser	Ile	Gln	Cys	Tyr	
1				5				10					15			
CTG	TGT	TTA	CTT	CTA	AAG	AGT	CAT	TTT	CTA	ACT	GAA	GCT	GGC	ATT	CAT	96

Leu Cys Leu Leu Leu Lys Ser His Phe Leu Thr Glu Ala Gln Ile His	20	25	30	
GTC TTC ATT TTG GGC TGT TTC AGT GCA GGG CTC CCT AAA ACA GAA GCC				144
Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala	35	40	45	
AAC TGG GTG AAT GTA ATA AGT GAT TTG AAA AAA ATT GAA GAT CTT ATT				192
Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile	50	55	60	
CAA TCT ATG CAT ATT GAT GCT ACT TTA TAT ACA GAA AGT GAT GTT CAC				240
Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His	65	70	75	80
CCC AGT TGC AAG GTA ACA GCA ATG AAG TGC TTT CTC TTG GAG TTG CAA				288
Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln	85	90	95	
GTT ATT TCA CAT GAG TCC GGA GAT ACA GAT ATT CAT GAT ACA GTA GAA				336
Val Ile Ser His Glu Ser Gly Asp Thr Asp Ile His Asp Thr Val Glu	100	105	110	
AAT CTT ATC ATC CTA GCA AAC AAC ATC TTG TCT TCT AAT GGG AAT ATA				384
Asn Leu Ile Ile Leu Ala Asn Asn Ile Leu Ser Ser Asn Gly Asn Ile	115	120	125	
ACA GAA TCT GGA TGC AAA GAA TGT GAG GAA CTA GAG GAA AAA AAT ATT				432
Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile	130	135	140	
AAA GAA TTT TTG CAG AGT TTT GTA CAT ATT GTC CAA ATG TTC ATC AAC				480
Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn	145	150	155	160
ACT TCT TGA				489
Thr Ser				

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 489 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATG AGA ATT TCG AAA CCA CAT TTG AGA AGT ATT TCC ATC CAG TGC TAC					48
Met Arg Ile Ser Lys Pro His Leu Arg Ser Ile Ser Ile Gln Cys Tyr	1	5	10	15	
TTG TGT TTA CTT CTA AAC AGT CAT TTT CTA ACT GAA GCT GGC ATT CAT					96
Leu Cys Leu Leu Leu Asn Ser His Phe Leu Thr Glu Ala Gly Ile His	20	25	30		
GTC TTC ATT TTG GGC TGT TTC AGT GCA GGG CTT CCT AAA ACA GAA GCC					144
Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala	35	40	45		

AAC TGG GTG AAT GTA ATA AGT GAT TTG AAA AAA ATT GAA GAT CTT ATT Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile 50 55 60	192
CAA TCT ATG CAT ATT GAT GCT ACT TTA TAT ACG GAA AGT GAT GTT CAC Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His 65 70 75 80	240
CCC AGT TGC AAA GTA ACA GCA ATG AAG TGC TTT CTC TTG GAG TTA CAA Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln 85 90 95	288
GTT ATT TCA CTT GAG TCC GGA GAT GCA AGT ATT CAT GAT ACA GTA GAA Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu 100 105 110	336
AAT CTG ATC ATC CTA GCA AAC AAC AGT TTG TCT TCT AAT GGG AAT GTA Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val 115 120 125	384
ACA GAA TCT GGA TGC AAA GAA TGT GAG GAA CTG GAG GAA AAA AAT ATT Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile 130 135 140	432
AAA GAA TTT TTG CAG AGT TTT GTA CAT ATT GTC CAA ATG TTC ATC AAC Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn 145 150 155 160	480
ACT TCT TGA Thr Ser	489

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AATGTAATAA GTTGTTTGAA AAAAATT

27

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AATGTAATAA GTTCTTTGAA AAAAATT

27

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTTGATGAAC ATGCAGACAA TATG

24

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTTGATGAAC ATAGAGACAA TATG

24

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTCCTCGCAA CTAAGTCGAC TAACTGGGTG AATGTAATA

39

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAGTCATTCT CGACTTGC GG CCGCACCAGA AGTGTGATG AACAT

45

~~(2) INFORMATION FOR SEQ ID NO:9:~~

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AATATGGTAC CTTTGGATAA AAGAGACTAC AAGGACGACG ATGACAAGAA

50

CTGGGTGAAT GTAATAAGT

69

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCGATATATC CATGGTCAAG AAGTGTTGAT GAACAT

36